Figure 1. Melting Curves for Genotyping the Most Stable Mismatch

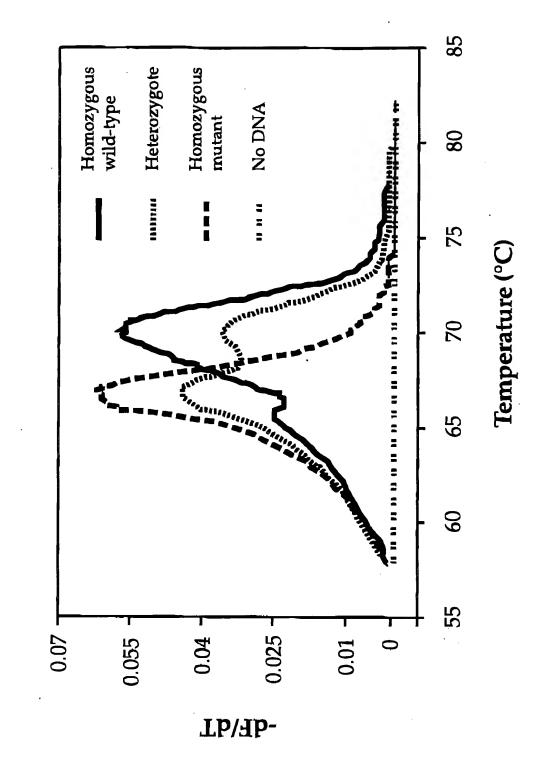
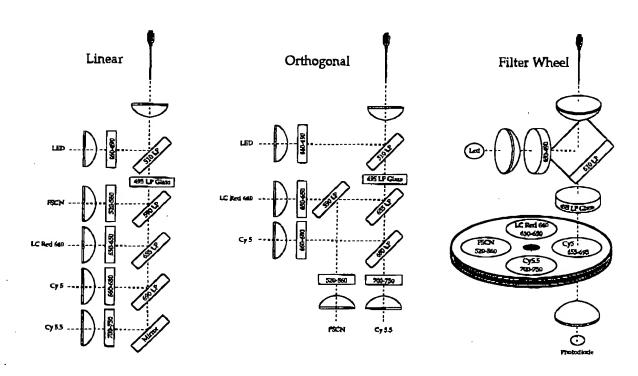


Figure 8. Four Color Light Cycler TM - Optical Design



Percent	of S	pectra	in	Band	Pass
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	FSCN	LC Red 640	Cy S	Cy 5.5
LED	47	8.0	0.2	0.3
FSCN	48	<0.1	<0.1	<0.1
LC Red 640	1.5	41	7.8	0.8
Cy 5	0,7	14	43	11
Cy 5.5	0.4	7.7	16	49

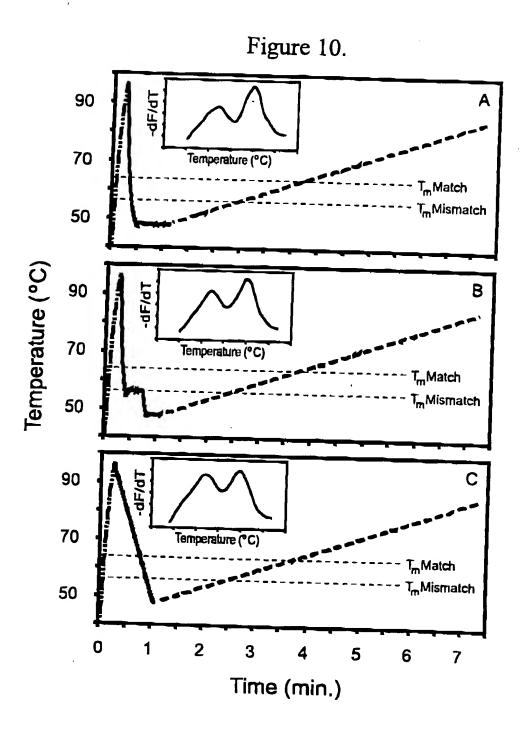
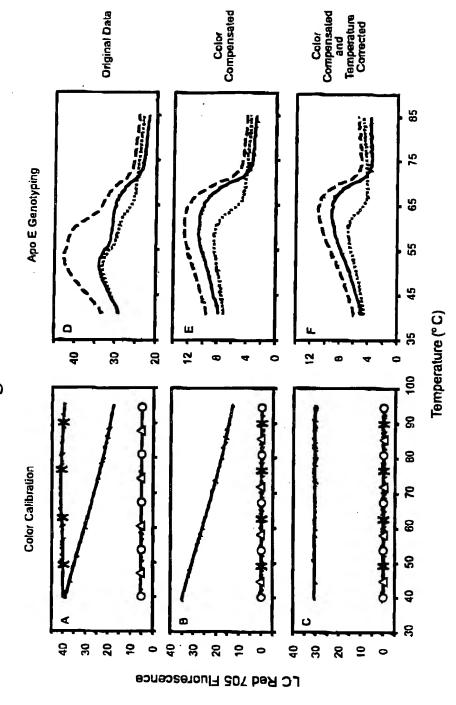
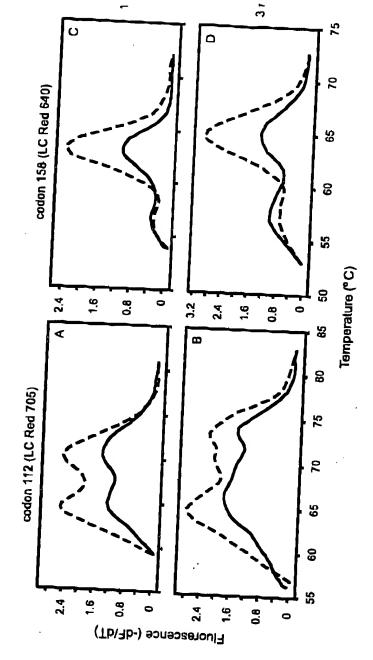


Figure 11.



APR. 19. 2002 8:59AM FLEHR HOHBACH TEST

Figure 12.



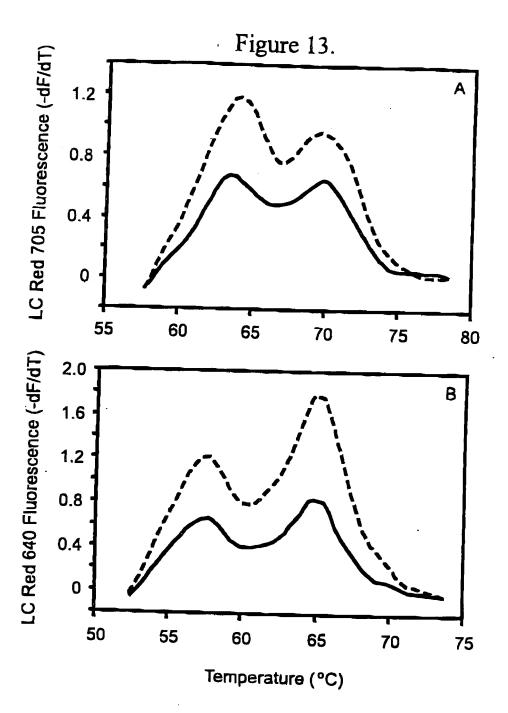


Figure 18.

Sequence Variation and Probe Design at HLA-A

CCGCGGGCRCCGTGGATAGRGCAGGAGRRKCCKGAGTATTGG	GACCAGGAGACACGGAATATGAAGGCCCACTCA GG A C G C AG G	Matched Allele
GECGCCCGGCACCTATCTCGTCCTCCCCGGCCTCATAACC	TGGTCCTCTGTGCCTTATACTTCCGGGTGAG	0101
Anchor Probe (Fluorescein)	TGCCCCTCTGTGCCTTACACTTCCGGGTGAG	0208
	Multicolored Probes	
(LCRod640)/		
I.C.Red705		

Figure 19. Predicted Tms for 2 Probes at a HLA-A Variable Reigon

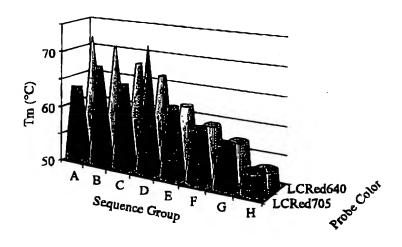


Figure 20. Sequence Variation and Probe Design at DRB1

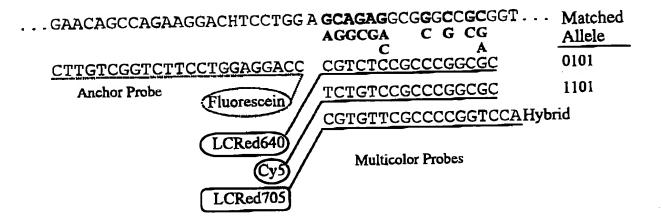


Figure 21. Predicted Tms for 3 Probes at a HLA DRB1 Variable Region

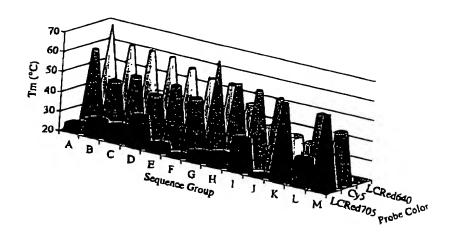


Figure 18.

Fig. 28. Sequence Variation and Probe Design at HLA-A

CCGCGGGCRCCGTGGATAGRGCAGGAGRRKCCKGAGTATTGGGACCAGGAGACAC GG A C G	GGAATATGAAGGCCCACTCA C AG G	Matched Allele
4-4 b-d-state margin and the state of the st	CCTTATACTTCCGGGTGAG	0101
Anchor Probe (Fluorescein) TGCCCCTCTGTG	CCTTACACTTCCGGGTGAG	0208
Multico	olored Probes	
(LCRed640)/		
LCRed705		

Figure 19. Predicted Tms for 2 Probes at a HLA-A Variable Reigon

	<u>}</u>	redicted	Probe Tr	n
Sequence	Frequency	LCRed	I Chad	_
Group HLA-A Alleles	(%)	640	705	
A 0101-0103 1106 3601	15.2	71.6	63.3	
B 3002-3006 3101 31-3 3104	6.2	70.3	67.6	
3201-3204 7401-7404 C 0301 0302 0304 0305	10.4			
D 0201 0202-0207 0209-0219 2408	13.4 27.2	67.8	65.0	
16 additional 0220	21.2	66.1	72.3	٠.
E 2301-2305 2402-2406 fladditional 2430	11.	61.6	62.5	
P 2901-2903 7 additional 68XX	3.6	58.9	59.6	
G 2501-2503 2601-2606 2608-2612 3301-33	05 7.2	56.8	57.8	
H 2502 2613 6601 6602 6801-6802 6901	-7	528	54.1	
Total Estimated Frequency	00.0	- 1		
25 25 25 25 25 25 25 25 25 25 25 25 25 2	90.9			
		_		•
70				
		-		
(C) 60 (B)		-		
50				
CD		7 00 4	4	
Sequence E F		LCRed6 CRed705	40 CD(0)	
Sequence Group F	3 H	~Ven \03	40 Color	
		1	\$7°	

Figure 21. Predicted Tms for 3 Probes at a HLA DRB1 Variable Region

1			Predic	ted Pro	be Tm	I .
Anonb		Frequency (%)	LCRed 640	Cy5	LCRed 705	
B C D E F G H I J K L M	0101 0404 0405 0408 0410 1072 1406 0801 0802 0803 0804 1501 1502 1503 0401 0901 1401 1404 100) 11011 11012 1104 1305 16012 16022 0103 0402 1102 1103 1301 1302 1304 1303 1301 1201 1202 16011 16021 0303 0407 0701 Total Estimated Frequency	15.8 4.1 13.6 6.4 3.8 9.9 7.5 13.1 1.2 4.5 10.1 2.0 8.2	69.5 61.2 60.9 60.1 57.1 54.5 54.1 46.4 97.4 35.5 34.4 29.3 <20.0	59.0 45.7 50.4 43.6 50.6 46.9 68.1 59.0 58.2 56.7 20.0 46.5		A B C D E F C H LCys Credo